IN THE SPECIFICATION

Please replace the paragraph beginning at line 2 of page 58 with the following amended paragraph:

5'-AGCGCTAACTGAGACNNNNNAGAGHHHHHGGHHHHHGGHHHHHG-GCTCGACATGCGTA-3' (SEQ ID NO:12)

Please replace the paragraph beginning at line 6 of page 58 with the following amended paragraph:

3'-TCGCGATTGACTCTGNNNNNT-5'-Sca(Y)$_3$ (SEQ ID NO:13)
(1024 different anti-codons possible)

Please replace the paragraph beginning at line 10 of page 58 with the following amended paragraph:

First building block:
FE_1-CTCDDDDDCC-5' (SEQ ID NO:14)

Please replace the paragraph beginning at line 14 of page 58 with the following amended paragraph:

FE_2-CTCIIIIICCDDDDDCC-5' (SEQ ID NO:15)

Please replace the paragraph beginning at line 17 of page 58 with the following amended paragraph:

FE_3-CTCIIIIICCIIIIICCDDDDDCC-5' (SEQ ID NO:16)

Please replace the paragraph beginning at line 28 of page 58 with the following amended paragraph:

- a first priming site (AGCGC TAACT GAGAC) (bases 1-15 of SEQ ID NO:12) which also serves as affinity providing sequence for the scaffold,
- a codon encoding the scaffold (NNNNN) (bases 16 to 20 of SEQ ID NO:12). N ~~may be~~ is selected as appropriate among the 4 naturally occurring nucleobases. Thus, in the generation of a library, a total of 4^5=1024 different variations exist.

Please replace the paragraph beginning at line 4 of page 59 with the following amended paragraph:

- a first building block codon (HHHHH) (bases 25 to 29 of SEQ ID NO:12). H ~~may be~~ is selected among the three nucleobases C, A, and T. Therefore, the total number of different combinations is 3^5=243.

Please replace the paragraph beginning at line 8 of page 59 with the following amended paragraph:

- a second building block codon (HHHHH) (bases 32 to 36 of SEQ ID NO:12). H ~~may be~~ is selected among the three nucleobases C, A, and T. Therefore, the total number of different combinations is 3^5=243.

Please replace the paragraph beginning at line 12 of page 59 with the following amended paragraph:

- A third building block codon (HHHHH) (bases 39 to 43 of SEQ ID NO:12). H ~~may be~~ is selected among the three nucleobases C, A, and T. Therefore, the total number of different combinations is 3^5=243.

Please replace the paragraph beginning at line 16 of page 59 with the following amended paragraph:

- A second priming site (GGCTCGACATGCGTA) (bases 44 to 58 of SEQ ID NO:12).

Please replace the paragraph beginning at line 23 of page 70 with the following amended paragraph:

This example describes the templated synthesis of a scaffolded molecule comprising 3 DNA encoded substituents using the set-up described in figure 1. A hexameric scaffold peptide with the sequence, CysPhePheLysLysLys (SEQ ID NO:17), was synthesised by standard solid-phase Fmoc peptide chemistry. The scaffold peptide comprises a -SH group on the cysteine side chain, said -SH group being used for coupling the scaffold

peptide to a amine-bearing oligonucleotide serving as a anticodon and linker. Each of the three lysine moieties comprises an amino group in the side chain. The amine groups are used as reactive groups for the formation of a connection to functional entities emanating from building blocks.

Please replace the paragraph beginning at line 11 of page 71 with the following amended paragraph:

5 nmol of oligodeoxynucleotide O1, YCGATGGATGCTCCAGGTCGC (SEQ ID NO:1) where Y=C6 amino-group (Glen Research, cat. #10-1039-90) in 100 mM Hepes-OH pH 7.5 is incubated with 20 mM Succinimidyl-propyl-2-dithiopyridyl (SPDP, Molecular probes) dissolved in DMSO for 3 hours at 25°C. Excess SPDP is removed by triple extraction using 5 volumes of ethylacetate. The sample is further purified using a Bio-rad Microspin 6 column equilibrated in H_2O.

Please replace the paragraph beginning at line 8 of page 72 with the following amended paragraph:

The three building block oligonucleotides O2, BGAGCATCCATCGX (SEQ ID NO:2), O3, BCTGGAGCATCCATCGX (SEQ ID NO:3) and O4, BGCGACCTGGAGCATCCATCGX (SEQ ID NO:4) each comprising a 5' biotin group (B) and a 3' end C6 S-S thiol modifier (X) (Glen Research #10-1936-90) was provided. Initially, a free thiol-group was formed in a reduction-step by incubating 10 nmol of each oligonucleotide with 100 mM DTT in a 100 mM sodium-phosphate buffer pH 8.0 at 37°C for 30 min. Subsequently, buffer and DTT are removed using Bio-rad Microspin 6 columns. Next, the free thiol-group was reacted with the Michael-acceptor of N-hydroxymaleimide to form the N-hydroxysuccinimid-oligo complex using the following procedure: The thiol-oligo is incubated in 100 mM Hepes-OH pH 7.5 and 100 mM N-hydroxymaleimide (Merck) at 25°C for 2 hours. Subsequently, buffer and excess NHM are removed using Bio-rad Microspin 6 columns. Synthesis of oligo-NHS complexes are verified by ES-MS.

Please replace the paragraph beginning at line 2 of page 75 with the following amended paragraph:

O5: GAG CAT CCA TCG-S-S (SEQ ID NO:5)

O6: CTG GAG CAT CCA TCG-S-S (SEQ ID NO:6)

O7: GCG ACC TGG AGC ATC CAT CG-S-S (SEQ ID NO:7)

O8: GAC GAG CAT CCA TCG-S-S (SEQ ID NO:8)

O9: CTA GGG ACG AGC ATC CAT CG-S-S (SEQ ID NO:9)

Please replace the paragraph beginning at line 4 of page 77 with the following amended paragraph:

The scheme below shows the Hexapeptide (Cys-Phe-Phe-Lys-Lys-Lys) (SEQ ID NO:17) used to load to an amino oligonucleotide to create an identifier molecule.

Please replace the paragraph beginning at line 15 of page 77 with the following amended paragraph:

Two 5' amino NH_2-oligonucleotides also coupled with a photocleavable linker (PC) and biotin in the 3' end were used to produce the templates. 10 nmol each of O10: NH2-CGA TGG ATG CTC CCA GGT CGC A-PC-Biotin (SEQ ID NO:10) and O11: NH2-CGA TGG ATG CTC GTC CCT AGA PC-Biotin (SEQ ID NO:11) was diluted in 160 µL 100 mM Hepes-KOH buffer pH 7.5 40 µl N-Succinimidyl 3-[2-pyridyldithio]-propionamido (Pierce cat #21857), a heterobifunctional cleavable cross-linker, was added to each oligonucleotide in an amount of 40 µl 20 mM and incubated for 2 h at 30°C. The oliognucleotides were ethylacetate extracted and purified using micro spin columns equilibrated with 100 mM Hepes-KOH buffer pH 7,5. 10 ul 100 mM template was added and incubated over-night at 30°C.